

RAW SEQUENCE LISTING

DATE: 12/06/2000

PATENT APPLICATION: US/09/549,848A

TIME: 19:23:16

Input Set : A:\Pto.amc

Output Set: N:\CRF3\12062000\I549848A.raw

P.S

```

4 <110> APPLICANT: Lassner, Michael
5   Post-Beittenmiller, Dusty
6   Savidge, Beth
7   Weiss, James
9 <120> TITLE OF INVENTION: Nucleic Acid Sequences Involved in
10  Tocopherol Synthesis
12 <130> FILE REFERENCE: 17133/02/US
14 <140> CURRENT APPLICATION NUMBER: 09/549,848A
15 <141> CURRENT FILING DATE: 2000-04-14
17 <150> PRIOR APPLICATION NUMBER: 60/129,899
18 <151> PRIOR FILING DATE: 1999-04-15
20 <150> PRIOR APPLICATION NUMBER: 60/146,461
21 <151> PRIOR FILING DATE: 1999-07-30
23 <160> NUMBER OF SEQ ID NOS: 94
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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28 <211> LENGTH: 1182
29 <212> TYPE: DNA
30 <213> ORGANISM: Arabidopsis sp
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35 aaagtgtgctg caaaaccgaa gtttaggaac aatcttggtt ggccctgatgg tcaaggatct      180
36 tcattgttgtt tgtatccaaa acataagtcg agatttcggg ttaatgccac tgcgggctcag      240
37 cctgagggctt tcgactcgaa tagcaaacag aagtctttta gagactcgtt agatgcggtt      300
38 tacagggtttt ctaggcctca tacagttatt ggcacagtgc ttageatttt atctgtatct      360
39 ttcttagcag tagagaaggt ttctgatata tctcctttac ttctcactgg catcttggag      420
40 gctgttggtt cagctctcat gatgaacatt tacatagttg ggctaaatca gttgtctgat      480
41 gttgaaatag ataaggttaa caagccctat ctccatttg catcaggaga atattctggt      540
42 aacaccggca ttgcaatagt agcttctctc tccatcatga gtttctggct tgggtggatt      600
43 gttggttcat ggccattggt ctgggctctt ttgttgagtt tcatgctcgg tactgcatac      660
44 tctatcaatt tgccactttt acggtggaaa agatttgcatt tggttgcagc aatgtgtatc      720
45 ctgcgtgtcc gagctattat tgttcaaatc gccttttatt tacatattca gacacatgtg      780
46 ttggaagac caatcttggt cactaggcct ctattttctg ccactgcggt tatgagcttt      840
47 ttctctgtcg ttattgcatt gtttaaggat atacctgata tcgaagggga taagatatct      900
48 ggaatccgat cattctctgt aactctgggt cagaaaacggg tgttttggac atgtgttaca      960
49 ctacttcaaa tggcttaacg tgttgcaatt ctagtggag ccacatctcc attcatatgg      1020
50 agcaaaagtc tctcggttgt gggtcattgt atactcgcaa caactttgtg ggctcgagct      1080
51 aagtcggttg atctgagtag caaaaccgaa ataacttcat gttatatgtt catatggaag      1140
52 ctcttttatg cagagtactt gctgttacct tttttgaagt ga      1182
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55 <211> LENGTH: 393
56 <212> TYPE: PRT
57 <213> ORGANISM: Arabidopsis sp
59 <400> SEQUENCE: 2
60 Met Glu Ser Leu Ser Ser Ser Ser Leu Val Ser Ala Ala Gly Gly
61  1          5          10          15

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62 Phe Cys Trp Lys Lys Gln Asn Leu Lys Leu His Ser Leu Ser Glu Ile
63           20           25           30
64 Arg Val Leu Arg Cys Asp Ser Ser Lys Val Val Ala Lys Pro Lys Phe
65           35           40           45
66 Arg Asn Asn Leu Val Arg Pro Asp Gly Gln Gly Ser Ser Leu Leu Leu
67           50           55           60
68 Tyr Pro Lys His Lys Ser Arg Phe Arg Val Asn Ala Thr Ala Gly Gln
69 65           70           75           80
70 Pro Glu Ala Phe Asp Ser Asn Ser Lys Gln Lys Ser Phe Arg Asp Ser
71           85           90           95
72 Leu Asp Ala Phe Tyr Arg Phe Ser Arg Pro His Thr Val Ile Gly Thr
73           100          105          110
74 Val Leu Ser Ile Leu Ser Val Ser Phe Leu Ala Val Glu Lys Val Ser
75           115          120          125
76 Asp Ile Ser Pro Leu Leu Phe Thr Gly Ile Leu Glu Ala Val Val Ala
77           130          135          140
78 Ala Leu Met Met Asn Ile Tyr Ile Val Gly Leu Asn Gln Leu Ser Asp
79 145          150          155          160
80 Val Glu Ile Asp Lys Val Asn Lys Pro Tyr Leu Pro Leu Ala Ser Gly
81           165          170          175
82 Glu Tyr Ser Val Asn Thr Gly Ile Ala Ile Val Ala Ser Phe Ser Ile
83           180          185          190
84 Met Ser Phe Trp Leu Gly Trp Ile Val Gly Ser Trp Pro Leu Phe Trp
85           195          200          205
86 Ala Leu Phe Val Ser Phe Met Leu Gly Thr Ala Tyr Ser Ile Asn Leu
87           210          215          220
88 Pro Leu Leu Arg Trp Lys Arg Phe Ala Leu Val Ala Ala Met Cys Ile
89 225          230          235          240
90 Leu Ala Val Arg Ala Ile Ile Val Gln Ile Ala Phe Tyr Leu His Ile
91           245          250          255
92 Gln Thr His Val Phe Gly Arg Pro Ile Leu Phe Thr Arg Pro Leu Ile
93           260          265          270
94 Phe Ala Thr Ala Phe Met Ser Phe Phe Ser Val Val Ile Ala Leu Phe
95           275          280          285
96 Lys Asp Ile Pro Asp Ile Glu Gly Asp Lys Ile Phe Gly Ile Arg Ser
97           290          295          300
98 Phe Ser Val Thr Leu Gly Gln Lys Arg Val Phe Trp Thr Cys Val Thr
99 305          310          315          320
100 Leu Leu Gln Met Ala Tyr Ala Val Ala Ile Leu Val Gly Ala Thr Ser
101           325          330          335
102 Pro Phe Ile Trp Ser Lys Val Ile Ser Val Val Gly His Val Ile Leu
103           340          345          350
104 Ala Thr Thr Leu Trp Ala Arg Ala Lys Ser Val Asp Leu Ser Ser Lys
105           355          360          365
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108 Glu Tyr Leu Leu Leu Pro Phe Leu Lys
109 385          390
111 <210> SEQ ID NO: 3

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112 <211> LENGTH: 1224
113 <212> TYPE: DNA
114 <213> ORGANISM: Arabidopsis sp
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119 actaccattt acacaaatcc tttcactaag tgttatectt catggaatga taattaccaa      180
120 gtatggagta aaggaagaga attgcatcag gagaagtttt ttggtgttgg ttggaattac      240
121 agattaattt gtggaatgtc gtcgtctctt tcggttttgg agggaaagcc gaagaaagat      300
122 gataaggaga agagtgtatg tgttgttgtt aagaaagctt cttggataga ttgtatttta      360
123 ccagaagaaag tttagaggtta tgctaagctt gctcgatttg ataaacccat tggaaacttg      420
124 ttgcttgctt ggccttctat gtgtctgatt gcgttggttg ctgaccttgy aagccttcca      480
125 agtttttaaat atatggcttt atttgggttc ggagcattac ttcttagagg tgcgtgttgt      540
126 actataaatg atctgcttga tcaggacata gatacaaaag ttgatcgtac aaaactaaga      600
127 cctatcgcca gtggtctttt gacaccattt caagggtatt gatttctcgg gctgcagttg      660
128 cttttagggt tagggattct tctccaactt aacaattaca gccgtgtttt aggggcttca      720
129 tctttgttac ttgtcttttc ctaccactt atgaagaggt ttacattttg gcctcaagcc      780
130 tttttagggt tgaccataaa ctggggagca ttggttaggt ggactgcagt taaagggaagc      840
131 atagcaccat ctattgtact cctctctat ctctcggag tctgctggac ccttgtttat      900
132 gatactattt atgcacatca ggacaaagaa gatgatgtaa aagttgttgt taaglcacaa      960
133 gcccttagat tcggtgataa tacaaagctt tggttactg gatttggcac agcatccata      1020
134 ggtttctctg cacttctctg attcagtgca gatctcgggt ggcaatatta cgcactactg      1080
135 gccgctgcat caggacagtt aggatggcaa atagggaacg ctgacttata atctggtgct      1140
136 gactgcagta gaaaatttgt gtcgaacaag tggtttgggt ctatttatatt tagtggagtt      1200
137 gtacttgtaa gaagttttca ataa      1224
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140 <211> LENGTH: 407
141 <212> TYPE: PRT
142 <213> ORGANISM: Arabidopsis sp
144 <400> SEQUENCE: 4
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149 His Lys Ser Leu Ser Asn Pro Val Thr Thr His Tyr Thr Asn Pro Phe
150 35 40 45
151 Thr Lys Cys Tyr Pro Ser Trp Asn Asp Asn Tyr Gln Val Trp Ser Lys
152 50 55 60
153 Gly Arg Glu Leu His Gln Glu Lys Phe Phe Gly Val Gly Trp Asn Tyr
154 65 70 75 80
155 Arg Leu Ile Cys Gly Met Ser Ser Ser Ser Ser Val Leu Glu Gly Lys
156 85 90 95
157 Pro Lys Lys Asp Asp Lys Glu Lys Ser Asp Gly Val Val Val Lys Lys
158 100 105 110
159 Ala Ser Trp Ile Asp Leu Tyr Leu Pro Glu Glu Val Arg Gly Tyr Ala
160 115 120 125
161 Lys Leu Ala Arg Leu Asp Lys Pro Ile Gly Thr Trp Leu Leu Ala Trp
162 130 135 140
163 Pro Cys Met Trp Ser Ile Ala Leu Ala Ala Asp Pro Gly Ser Leu Pro

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DEC 11 2000

TECH CENTER 1600/2900

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Input Set : A:\Pto.amc

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164	145				150					155				160		
165	Ser	Phe	Lys	Tyr	Met	Ala	Leu	Phe	Gly	Cys	Gly	Ala	Leu	Leu	Leu	Arg
166					165					170						175
167	Gly	Ala	Gly	Cys	Thr	Ile	Asn	Asp	Leu	Leu	Asp	Gln	Asp	Ile	Asp	Thr
168					180					185						190
169	Lys	Val	Asp	Arg	Thr	Lys	Leu	Arg	Pro	Ile	Ala	Ser	Gly	Leu	Leu	Thr
170					195					200						205
171	Pro	Phe	Gln	Gly	Ile	Gly	Phe	Leu	Gly	Leu	Gln	Leu	Leu	Gly	Leu	
172					210					215						220
173	Gly	Ile	Leu	Leu	Gln	Leu	Asn	Asn	Tyr	Ser	Arg	Val	Leu	Gly	Ala	Ser
174	225									230						240
175	Ser	Leu	Leu	Leu	Val	Phe	Ser	Tyr	Pro	Leu	Met	Lys	Arg	Phe	Thr	Phe
176					245					250						255
177	Trp	Pro	Gln	Ala	Phe	Leu	Gly	Leu	Thr	Ile	Asn	Trp	Gly	Ala	Leu	Leu
178					260					265						270
179	Gly	Trp	Thr	Ala	Val	Lys	Gly	Ser	Ile	Ala	Pro	Ser	Ile	Val	Leu	Pro
180					275					280						285
181	Leu	Tyr	Leu	Ser	Gly	Val	Cys	Trp	Thr	Leu	Val	Tyr	Asp	Thr	Ile	Tyr
182					290					295						300
183	Ala	His	Gln	Asp	Lys	Glu	Asp	Asp	Val	Lys	Val	Gly	Val	Lys	Ser	Thr
184	305									310						320
185	Ala	Leu	Arg	Phe	Gly	Asp	Asn	Thr	Lys	Leu	Trp	Leu	Thr	Gly	Phe	Gly
186					325					330						335
187	Thr	Ala	Ser	Ile	Gly	Phe	Leu	Ala	Leu	Ser	Gly	Phe	Ser	Ala	Asp	Leu
188					340					345						350
189	Gly	Trp	Gln	Tyr	Tyr	Ala	Ser	Leu	Ala	Ala	Ser	Gly	Gln	Leu	Gly	
190					355					360						365
191	Trp	Gln	Ile	Gly	Thr	Ala	Asp	Leu	Ser	Ser	Gly	Ala	Asp	Cys	Ser	Arg
192					370					375						380
193	Lys	Phe	Val	Ser	Asn	Lys	Trp	Phe	Gly	Ala	Ile	Ile	Phe	Ser	Gly	Val
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206	cctccgggtct	cgacgggaatc	aactgctaag	ttagggatca	ctgggtgttag	atctgatgcc										180
207	aategagttt	ttgccactgc	tactgccgcc	gctacagcta	cagctaccac	cggtgagatt										240
208	tctgtctagag	ttgcggcttt	ggctggatta	gggcatcact	acgctcgttg	ttattgggag										300
209	ctttctaaag	ctaaacttag	tatgcttgtg	gttgcaactt	ctggaaactgg	gtatatctctg										360
210	ggtacgggaa	atgctgcaat	tagcttcccg	gggcttttgt	acacatgtgc	aggaaccatg										420
211	atgattgctg	catctgctaa	ttccttgaat	cagatttttg	agataagcaa	tgattctaag										480
212	atgaaaagaa	cgatgctaag	gccattgcct	tcaggacgta	ttagtgttcc	acacgctggt										540
213	gcattgggcta	ctattgctgg	tgcctctggg	gcttggttgt	tggccagcaa	gactaatatg										600
214	ttggctgctg	gacttgcatc	tgccaatctt	gtactttatg	cgtttggtta	tactccgittg										660

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215 aagcaacttc accctatcaa tacatgggtt ggcgctgttg ttggtgctat cccacccttg      720
216 cttgggtggg cggcagcgtc tggtcagatt tcatacaatt cgatgattct tccagctgct      780
217 ctttactttt qgcagatacc tcattttatg gcccttgcac atctctgccg caatgattat      840
218 gcagctggag gttacaagat gttgtcactc ttgtatccct cagggaagag aatagcagca      900
219 gtggctctaa ggaactgctt ttacatgata cctctcggtt tcctcgcta tgactggggg      960
220 tlaacctcaa gttggttttg cctcgaatca acacttctca cactagcaat cgctgcaaca     1020
221 qcattttcat tctaccgaqa ccggaccatg cataaagcaa ggaataatgtt ccatgccaat     1080
222 cttctcttcc ttctgtttt catgtctggt cttcttctac accgtgtctc taatgataat     1140
223 cagcaacaac tctagaaga agccggatta acaaatcttg tatctggtga agtcaaaact     1200
224 cagaggcgaa agaaacgtgt ggtcaacct ccggtggctt atgacctctg tgcaccgttt     1260
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228 <211> LENGTH: 431
229 <212> TYPE: PRT
230 <213> ORGANISM: Arabidopsis sp
232 <400> SEQUENCE: 6
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237 Cys Ala Val Asn Ser Phe Ser Gln Pro Pro Val Ser Thr Glu Ser Thr
238 35 40 45
239 Ala Lys Leu Gly Ile Thr Gly Val Arg Ser Asp Ala Asn Arg Val Phe
240 50 55 60
241 Ala Thr Ala Thr Ala Ala Thr Ala Thr Thr Thr Gly Glu Ile
242 65 70 75 80
243 Ser Ser Arg Val Ala Ala Leu Ala Gly Leu Gly His His Tyr Ala Arg
244 85 90 95
245 Cys Tyr Trp Glu Leu Ser Lys Ala Lys Leu Ser Met Leu Val Val Ala
246 100 105 110
247 Thr Ser Gly Thr Gly Tyr Ile Leu Gly Thr Gly Asn Ala Ala Ile Ser
248 115 120 125
249 Phe Pro Gly Leu Cys Tyr Thr Cys Ala Gly Thr Met Met Ile Ala Ala
250 130 135 140
251 Ser Ala Asn Ser Leu Asn Gln Ile Phe Glu Ile Ser Asn Asp Ser Lys
252 145 150 155 160
253 Met Lys Arg Thr Met Leu Arg Pro Leu Pro Ser Gly Arg Ile Ser Val
254 165 170 175
255 Pro His Ala Val Ala Trp Ala Thr Ile Ala Gly Ala Ser Gly Ala Cys
256 180 185 190
257 Leu Leu Ala Ser Lys Thr Asn Met Leu Ala Ala Gly Leu Ala Ser Ala
258 195 200 205
259 Asn Leu Val Leu Tyr Ala Phe Val Tyr Thr Pro Leu Lys Gln Leu His
260 210 215 220
261 Pro Ile Asn Thr Trp Val Gly Ala Val Val Gly Ala Ile Pro Pro Leu
262 225 230 235 240
263 Leu Gly Trp Ala Ala Ala Ser Gly Gln Ile Ser Tyr Asn Ser Met Ile
264 245 250 255
265 Leu Pro Ala Ala Leu Tyr Phe Trp Gln Ile Pro His Phe Met Ala Leu

```

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\Pto.amc

Output Set: N:\CRF3\12062000\I549848A.raw

L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:680 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:681 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:760 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:790 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27